

Claims

We claim:

1. An array comprising polynucleotide probes, capable of hybridizing to nucleic acid
5 molecules of more than one of the genes in Table 1, 2, 4, and/or 5, hybridized to nucleic acids
derived from one or more ER+ breast cancer cell.
2. The array of claim 1 comprising 11 of the genes in Tables 1, 2, and/or 4.
3. The array of claim 2 comprising more than 11 of the genes.
4. The array of claim 1 wherein said one or more ER+ cell is a human cell.
- 10 5. The array of claim 1 wherein said nucleic acids derived from one or more ER+ cells
are prepared by mRNA amplification or quantitative PCR.
6. The array of claim 1 wherein said one or more ER+ cells are from a section of tissue
from a subject or are microdissected from said section.
7. A method to determine the survival outcome of an ER+ breast cancer afflicted
15 subject if treated with tamoxifen, said method comprising assaying a sample of ER+ breast cancer
cells from said subject for the expression level(s) of one or more genes in Table 1, 2, 4, and/or 5.
8. The method of claim 7 wherein said one or more genes is 11 or more genes.
9. The method of claim 7 wherein said subject is human.
10. The method of claim 7 wherein said assaying for the expression level of one or more
20 genes comprises detection of nucleic acids derived from said sample of ER+ breast cancer cells.

11. The method of claim 10 wherein said nucleic acids derived from said sample are prepared by mRNA amplification or quantitative PCR.

12. The method of claim 7 wherein said assaying for the expression level of one or more genes comprises detection of proteins encoded by said genes.

5 13. The method of claim 12 wherein said detection of proteins comprises detection with antibodies which bind said proteins.

14. A method of determining prognosis of a subject having ER+ breast cancer if treated with tamoxifen, or of a subject afflicted with ER+ breast cancer and treated with tamoxifen, said method comprising:

10 assaying for the expression level(s) of one or more genes in Table 1, 2, 4, and/or 5 from a breast cancer cell sample from said subject.

15. The method of claim 14 wherein said one or more genes is 11 or more genes.

16. The method of claim 14 wherein said subject is human.

17. The method of claim 14 wherein said assaying for the expression level of one or
15 more genes comprises detection of nucleic acids derived from said sample of ER+ breast cancer cells or detection of proteins encoded by said genes.

18. The method of claim 17 wherein said nucleic acids derived from said sample are prepared by mRNA amplification or quantitative PCR.

19. The method of claim 17 wherein said detection of proteins comprises detection with
20 antibodies which bind said proteins.

20. The method of claim 14 wherein said assaying comprises using an array.

21. The method of claim 14 wherein said sample is a ductal lavage or fine needle aspiration sample.

22. The method of claim 14 wherein said sample is a section of tissue from a subject or
5 are cells microdissected from said section.

23. A method to determine therapeutic treatment for an ER+ breast cancer patient based upon said patient's expected response to tamoxifen treatment, said method comprising
determining an expected response to tamoxifen treatment for said patient by assaying a
10 sample of breast cancer cells from said patient for the expression level(s) of one or more one genes in Table 1, 2, 4, and/or 5; and
selecting the appropriate treatment for a patient with such a survival outcome.

24. The method of claim 23 wherein said one or more genes is 11 or more genes.

25. The method of claim 23 wherein said subject is human.

15 26. The method of claim 23 wherein said assaying comprises detection of nucleic acids derived from said sample of ER+ breast cancer cells or detection of proteins encoded by said genes.

27. The method of claim 26 wherein said nucleic acids derived from said sample are prepared by mRNA amplification or quantitative PCR.

28. The method of claim 26 wherein said detection of proteins comprises detection with
20 antibodies which bind said proteins.

29. The method of claim 23 wherein said assaying comprises using an array.

30. The method of claim 23 wherein said sample is a ductal lavage or fine needle aspiration sample.

31. The method of claim 23 wherein said sample is a section of tissue from a subject or are cells microdissected from said section.

5 32. A method to determine the survival outcome of a human subject having ER+ breast cancer if treated with tamoxifen, said method comprising assaying a sample of breast cells from said subject for increased expression of one or more human IL17RB or CACNA1D sequences.

33. The method of claim 32 wherein said sample is obtained by solid tissue biopsy or a non-invasive procedure, such as ductal lavage, fine needle aspiration, or a needle biopsy.

10 34. The method of claim 33 wherein microdissection is used to isolate breast cells from said sample before assaying for nucleic acid expression.

35. The method of claim 32 wherein said assaying is by hybridization to a polynucleotide comprising sequences of at least 24 nucleotides from the 3' untranslated region, the coding region, or the 5' untranslated region, of human IL17RB or CACNA1D.

15 36. The method of claim 32 wherein said assaying comprises mRNA amplification or PCR amplification, such as quantitative PCR, of said sequences.

37. The method of claim 32 wherein said assaying for increased expression comprises detection of polypeptides encoded by said sequences.

38. The method of claim 37 wherein said detection of polypeptides comprises detection with antibodies which bind said polypeptides.

20 39. A method to determine the survival outcome of a human subject having ER+ breast cancer if treated with tamoxifen, said method comprising assaying a sample of breast cells from said subject for decreased expression of human HOXB13 sequences.

40. The method of claim 39 wherein said sample is obtained by solid tissue biopsy or a non-invasive procedure, such as ductal lavage, fine needle aspiration, or a needle biopsy.

41. The method of claim 40 wherein microdissection is used to isolate breast cells from said sample before assaying for nucleic acid expression.

5 42. The method of claim 39 wherein said assaying is by hybridization to a polynucleotide comprising sequences of at least 24 nucleotides from the 3' untranslated region, the coding region, or the 5' untranslated region, of human HOXB13.

43. The method of claim 39 wherein said assaying comprises mRNA amplification or PCR amplification, such as quantitative PCR, of said sequences.

10 44. The method of claim 39 wherein said assaying is for inactivation or methylation of HOXB13 sequences.

45. The method of claim 39 wherein said assaying comprises detection of increased mRNA degradation.

15 46. The method of claim 39 wherein said assaying for increased expression comprises detection of polypeptides encoded by said sequences.

47. The method of claim 46 wherein said detection of polypeptides comprises detection with antibodies which bind said polypeptides.

20 48. A population of singled stranded nucleic acid molecules comprising one or both strands of a human IL17RB or CACNA1D or HOXB13 sequence wherein at least a portion of said population is hybridized to one or both strands of a nucleic acid molecule quantitatively amplified from RNA of an ER+ breast cell.

49. The population of claim 48 wherein the population is immobilized on a solid support, such as a microarray.

50. The population of claim 48 wherein said nucleic acid molecules amplified from an ER+ breast cell are amplified by quantitative PCR (Q-PCR).

5 51. The population of claim 50 wherein said quantitative PCR is of amplified mRNA from said breast cancer cell.

52. The population of claim 48 wherein said population of single stranded molecules is equal to or in excess of all of one or both strands of the nucleic acid molecules amplified from an ER+ breast cell such that the population is sufficient to hybridize to all of one or both strands.

10 53. The population of claim 48 wherein said population of single stranded molecules comprising sequences of at least 24 nucleotides from the 3' untranslated region, the coding region, or the 5' untranslated region, of human IL17RB or CACNA1D or HOXB13.

15 54. A method to determine the survival outcome of a human subject having ER+ breast cancer if treated with tamoxifen, said method comprising assaying a sample of breast cells from said subject for increased expression of a sequence selected from SEQ ID NOS: 8, 9, or 11-17.

55. A method to determine the survival outcome of a human subject having ER+ breast cancer if treated with tamoxifen, said method comprising assaying a sample of breast cells from said subject for decreased expression of a sequence selected from SEQ ID NOS: 10 or 18-31.